

SEQUENCE LISTING

<110> KAPELLER-LIBERMANN
SILOS-SANTIAGO

<120> METHODS OF USING 18903 TO TREAT PAIN AND
PAIN-RELATED DISORDERS

<130> MNI-199

<150> 60/250929
<151> 2000-11-30

<160> 7

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (98)...(1849)

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Met Pro Ser Thr Val Leu
1 5
cca tcc aca gtg ttg cca tca ctc ctg ccc aca gca gga gct ggc tgg 163
Pro Ser Thr Val Leu Pro Ser Leu Leu Pro Thr Ala Gly Ala Gly Trp
10 15 20
gcg atg agg tgg att ctg tgc tgg agc ctc acc ctc tgc ctg atg gcg 211
Ser Met Arg Trp Ile Leu Cys Trp Ser Leu Thr Leu Cys Leu Met Ala
25 30 35
cag acg gcc ttg ggt gcc ttg cac acc aag agg cct caa gtg gtc acc 259
Gln Thr Ala Leu Gly Ala Leu His Thr Lys Arg Pro Gln Val Val Thr
40 45 50
aaa tat gga acc ctg caa gga aaa cag atg cat gtg ggg aag aca ccc 307
Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met His Val Gly Lys Thr Pro
55 60 65 70
atc caa gtc ttt tta gga gtc ccc ttc tcc aga cct cct cta ggt atc 355
Ile Gln Val Phe Leu Gly Val Pro Phe Ser Arg Pro Pro Leu Gly Ile
75 80 85
ctc agg ttt gca cct cca gaa ccc ccg gag ccc tgg aaa gga atc aga 403
Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu Pro Trp Lys Gly Ile Arg
90 95 100
gat gct acc acc tac ccg cct ggg tgc ctg cag gag tcc tgg ggc cag 451
Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu Gln Glu Ser Trp Gly Gln
105 110 115

ctg gcc tcg atg tac gtc agc acg cg ^g gaa cg ^g tac aag tgg ctg cgc	499
Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg Tyr Lys Trp Leu Arg	
120 125 130	
ttc agc gag gac tgt ctg tac ctg aac gtg tac g ^c cg ^g cg ^c cg ^c g ^c	547
Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val Tyr Ala Pro Ala Arg Ala	
135 140 145 150	
ccc ggg gat ccc cag ctg cca gtg atg gt ^c tgg ttc cg ^g gga gg ^c gg ^c	595
Pro Gly Asp Pro Gln Leu Pro Val Met Val Trp Phe Pro Gly Gly Ala	
155 160 165	
ttc atc gtg ggc gct gct tct tcg tac gag ggc tct gac ttg gcc gcc	643
Phe Ile Val Gly Ala Ala Ser Ser Tyr Glu Gly Ser Asp Leu Ala Ala	
170 175 180	
cgc gag aaa gtg gtg ctg gtg ttt ctg cag cac agg ctc gg ^c atc tt ^c	691
Arg Glu Lys Val Val Leu Val Phe Leu Gln His Arg Leu Gly Ile Phe	
185 190 195	
ggc ttc ctg agc acg gac gac agc cac gg ^c cg ^c ggg aac tgg ggg ctg	739
Gly Phe Leu Ser Thr Asp Asp Ser His Ala Arg Gly Asn Trp Gly Leu	
200 205 210	
ctg gac cag atg gg ^c gct ctg cg ^c tgg gtg cag gag aac atc gca gg ^c	787
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215 220 225 230	
ttc ggg gga gac cca gga aat gtg acc ctg ttc gg ^c cag tcg gg ^c ggg	835
Phe Gly Gly Asp Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly	
235 240 245	
ggc atg agc atc tca gga ctg atg atg tca ccc cta gg ^c tcg ggt ctc	883
Ala Met Ser Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu	
250 255 260	
ttc cat cgg gcc att tcc cag agt gg ^c acc gg ^c tta ttc aga ctt tt ^c	931
Phe His Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe	
265 270 275	
atc act agt aac cca ctg aaa gtg gg ^c aag aag gtt gg ^c cac ctg gct	979
Ile Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	
280 285 290	
gga tgc aac cac aac agc aca cag atc ctg gta aac tgc ctg agg gca	1027
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg Ala	
295 300 305 310	
cta tca ggg acc aag gtg atg cgt gtg tcc aac aag atg aga tt ^c ctc	1075
Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg Phe Leu	
315 320 325	
caa ctg aac ttc cag aga gac cc ^g gaa gag att atc tgg tcc atg agc	1123
Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp Ser Met Ser	
330 335 340	
cct gtg gtg gat ggt gtg gtg atc cca gat gac cct tt ^c gtg ctc ctg	1171
Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro Leu Val Leu Leu	
345 350 355	
acc cag ggg aag gtt tca tct gtg ccc tac ctt cta ggt gtc aac aac	1219

Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu Leu Gly Val Asn Asn			
360	365	370	
ctg gaa ttc aat tgg ctc ttg cct tat atc atg aag ttc ccg cta aac			1267
Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile Met Lys Phe Pro Leu Asn			
375	380	385	390
cgg cag gcg atg aga aag gaa acc atc act aag atg ctc tgg agt acc			1315
Arg Gln Ala Met Arg Lys Glu Thr Ile Thr Lys Met Leu Trp Ser Thr			
395	400	405	
cgc acc ctg ttg aat atc acc aag gag cag gta cca ctt gtg gtg gag			1363
Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu			
410	415	420	
gag tac ctg gac aat gtc aat gag cat gac tgg aag atg cta cga aac			1411
Glu Tyr Leu Asp Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn			
425	430	435	
cgt atg atg gac ata gtt caa gat gcc act ttc gtg tat gcc aca ctg			1459
Arg Met Met Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu			
440	445	450	
cag act gct cac tac cac cga gat gcc ggc ctc cct gtc tac ctg tat			1507
Gln Thr Ala His Tyr His Arg Asp Ala Gly Leu Pro Val Tyr Leu Tyr			
455	460	465	470
gaa ttt gag cac cac gct cgt gga ata atc gtc aaa ccc cgc act gat			1555
Glu Phe Glu His His Ala Arg Gly Ile Ile Val Lys Pro Arg Thr Asp			
475	480	485	
ggg gca gac cat ggg gat gag atg tac ttc ctc ttt ggg ggc ccc ttc			1603
Gly Ala Asp His Gly Asp Glu Met Tyr Phe Leu Phe Gly Gly Pro Phe			
490	495	500	
gcc aca ggc ctt tcc atg ggt aag gag aag gca ctt agc ctc cag atg			1651
Gly Ala Thr Gly Leu Ser Met Gly Lys Glu Lys Ala Leu Ser Leu Gln Met			
505	510	515	
atg aaa tac tgg gcc aac ttt gcc cgc aca gga aac ccc aat gat ggg			1699
Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr Gly Asn Pro Asn Asp Gly			
520	525	530	
aat ctg ccc tgc tgg cca cgc tac aac aag gat gaa aag tac ctg cag			1747
Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys Asp Glu Lys Tyr Leu Gln			
535	540	545	550
ctg gat ttt acc aca aga gtg ggc atg aag ctc aag gag aag aag atg			1795
Leu Asp Phe Thr Thr Arg Val Gly Met Lys Leu Lys Glu Lys Lys Met			
555	560	565	
gct ttt tgg atg agt ctg tac cag tct caa aga cct gag aag cag agg			1843
Ala Phe Trp Met Ser Leu Tyr Gln Ser Gln Arg Pro Glu Lys Gln Arg			
570	575	580	
caa ttc taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc			1899
Gln Phe			
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attcgtttaa acctgcagga ctag			1983

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<212> PRT
<213> Homo sapiens

<400> 2

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Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
35 40 45
Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
50 55 60
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
65 70 75 80
Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
85 90 95
Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
100 105 110
Gln Glu Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu
115 120 125
Arg Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val
130 135 140
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met Val
145 150 155 160
Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser Tyr Glu
165 170 175
Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val Phe Leu Gln
180 185 190
His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp Asp Ser His Ala
195 200 205
Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala Ala Leu Arg Trp Val
210 215 220
Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp Pro Gly Asn Val Thr Leu
225 230 235 240
Phe Gly Gln Ser Ala Gly Ala Met Ser Ile Ser Gly Leu Met Met Ser
245 250 255
Pro Leu Ala Ser Gly Leu Phe His Arg Ala Ile Ser Gln Ser Gly Thr
260 265 270
Ala Leu Phe Arg Leu Phe Ile Thr Ser Asn Pro Leu Lys Val Ala Lys
275 280 285
Lys Val Ala His Leu Ala Gly Cys Asn His Asn Ser Thr Gln Ile Leu
290 295 300
Val Asn Cys Leu Arg Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser
305 310 315 320
Asn Lys Met Arg Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu
325 330 335
Ile Ile Trp Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp
340 345 350
Asp Pro Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr
355 360 365
Leu Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Ile
370 375 380
Met Lys Phe Pro Leu Asn Arg Gln Ala Met Arg Lys Glu Thr Ile Thr
385 390 395 400
Lys Met Leu Trp Ser Thr Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln
405 410 415
Val Pro Leu Val Val Glu Glu Tyr Leu Asp Asn Val Asn Glu His Asp
420 425 430

Trp Lys Met Leu Arg Asn Arg Met Met Asp Ile Val Gln Asp Ala Thr
 435 440 445
 Phe Val Tyr Ala Thr Leu Gln Thr Ala His Tyr His Arg Asp Ala Gly
 450 455 460
 Leu Pro Val Tyr Leu Tyr Glu Phe Glu His His Ala Arg Gly Ile Ile
 465 470 475 480
 Val Lys Pro Arg Thr Asp Gly Ala Asp His Gly Asp Glu Met Tyr Phe
 485 490 495
 Leu Phe Gly Gly Pro Phe Ala Thr Gly Leu Ser Met Gly Lys Glu Lys
 500 505 510
 Ala Leu Ser Leu Gln Met Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr
 515 520 525
 Gly Asn Pro Asn Asp Gly Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys
 530 535 540
 Asp Glu Lys Tyr Leu Gln Leu Asp Phe Thr Thr Arg Val Gly Met Lys
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 Arg Pro Glu Lys Gln Arg Gln Phe
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1752)

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 aca gca gga gct ggc tgg agc atg agg tgg att ctg tgc tgg agc ctc 96
 Thr Ala Gly Ala Gly Trp Ser Met Arg Trp Ile Leu Cys Trp Ser Leu
 20 25 30
 acc ctc tgc ctg atg gcg cag acg gcc ttg ggt gcc ttg cac acc aag 144
 Thr Leu Cys Leu Met Ala Gln Thr Ala Leu Gly Ala Leu His Thr Lys
 35 40 45
 agg cct caa gtg gtc acc aaa tat gga acc ctg caa gga aaa cag atg 192
 Arg Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 50 55 60
 cat gtg ggg aag aca ccc atc caa gtc ttt tta gga gtc ccc ttc tcc 240
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe Ser
 65 70 75 80
 aga cct cct cta ggt atc ctc agg ttt gca cct cca gaa ccc ccg gag 288
 Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro Pro Glu
 85 90 95
 ccc tgg aaa gga atc aga gat gct acc acc tac ccg cct ggg tgc ctg 336
 Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro Gly Cys Leu
 100 105 110
 cag gag tcc tgg ggc cag ctg gcc tcg atg tac gtc agc acg cgg gaa 384

Gln	Glu	Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu		
115					120						125						
cgg	tac	aag	tgg	ctg	cgc	ttc	agc	gag	gac	tgt	ctg	tac	ctg	aac	gtg	432	
Arg	Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val		
130				135						140							
tac	gcf	ccg	cgf	cgf	ccc	ggg	gat	ccc	cag	ctg	cca	gtg	atg	gtc		480	
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	Val		
145				150					155				160				
tgg	ttc	ccg	gga	ggc	gcc	ttc	atc	gtg	ggc	gct	gtc	tct	tcg	tac	gag	528	
Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	Tyr	Glu		
165				170					175								
ggc	tct	gac	ttg	gcc	gcc	cgf	gag	aaa	gtg	gtg	ctg	gtg	ttt	ctg	cag		576
Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	Phe	Leu	Gln		
180				185					190								
cac	agg	ctc	ggc	atc	ttc	ggc	ttc	ctg	agc	acg	gac	agc	cac	gcf		624	
His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	Asp	Ser	His	Ala		
195				200					205								
cgc	ggg	aac	tgg	ggg	ctg	ctg	gac	cag	atg	gcf	gct	ctg	cgc	tgg	gtg	672	
Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	Ala	Leu	Arg	Trp	Val		
210				215					220								
cag	gag	aac	atc	gca	gcc	ttc	ggg	gga	gac	cca	gga	aat	gtg	acc	ctg	720	
Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Asn	Val	Thr	Leu		
225				230					235			240					
ttc	ggc	cag	tcg	ggg	gcc	atg	agc	atc	tca	gga	ctg	atg	atg	tca		768	
Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	Ile	Ser	Gly	Ile	Met	Met	Ser		
245					250					255							
ccc	cta	gcc	tcg	ggf	ctc	ttc	cat	cgf	gcc	att	tcc	cag	agt	ggc	acc	816	
Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr		
260				265					270								
gcg	tta	ttc	aga	ctt	ttc	atc	act	agt	aac	cca	ctg	aaa	gtg	gcc	aag	864	
Ala	Leu	Phe	Arg	Leu	Phe	Ile	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys			
275				280					285								
aag	gtt	gcc	cac	ctg	gct	gga	tgc	aac	cac	aac	agc	aca	cag	atc	ctg	912	
Lys	Val	Ala	His	Leu	Ala	Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu		
290				295					300								
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Val	Asn	Cys	Leu	Arg	Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser		
305				310					315			320					
aac	aag	atg	aga	ttc	ctc	caa	ctg	aac	ttc	cag	aga	gac	ccg	gaa	gag	1008	
Asn	Lys	Met	Arg	Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu		
325					330					335							
att	atc	tgg	tcc	atg	agc	cct	gtg	gtg	gat	ggt	gtg	atc	cca	gat		1056	
Ile	Ile	Trp	Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp		
340				345						350							
gac	cct	ttg	gtg	ctc	ctg	acc	cag	ggg	aag	gtt	tca	tct	gtg	ccc	tac	1104	
Asp	Pro	Leu	Val	Leu	Leu	Thr	Gln	Gly	Lys	Val	Ser	Ser	Val	Pro	Tyr		

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aag atg ctc tgg agt acc cgc acc ctg ttg aat atc acc aag gag cag Lys Met Leu Trp Ser Thr Arg Thr Leu Leu Asn Ile Thr Lys Glu Gln 405 410 415			1248
gta cca ctt gtg gtg gag gag tac ctg gac aat gtc aat gag cat gac Val Pro Leu Val Val Glu Glu Tyr Leu Asp Asn Val Asn Glu His Asp 420 425 430			1296
tgg aag atg cta cga aac cgt atg atg gac ata gtt caa gat gcc act Trp Lys Met Leu Arg Asn Arg Met Met Asp Ile Val Gln Asp Ala Thr 435 440 445			1344
ttc gtg tat gcc aca ctg cag act gct cac tac cac cga gat gcc ggc Phe Val Tyr Ala Thr Leu Gln Thr Ala His Tyr His Arg Asp Ala Gly 450 455 460			1392
ctc cct gtc tac ctg tat gaa ttt gag cac cac gct cgt gga ata atc Leu Pro Val Tyr Leu Tyr Glu Phe Glu His His Ala Arg Gly Ile Ile 465 470 475 480			1440
gtc aaa ccc cgc act gat ggg gca gac cat ggg gat gag atg tac ttc Val Lys Pro Arg Thr Asp Gly Ala Asp His Gly Asp Glu Met Tyr Phe 485 490 495			1488
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gca ctt agc ctc cag atg atg aaa tac tgg gcc aac ttt gcc cgc aca Ala Leu Ser Leu Gln Met Met Lys Tyr Trp Ala Asn Phe Ala Arg Thr 515 520 525			1584
gga aac ccc aat gat ggg aat ctg ccc tgc tgg cca cgc tac aac aag Gly Asn Pro Asn Asp Gly Asn Leu Pro Cys Trp Pro Arg Tyr Asn Lys 530 535 540			1632
gat gaa aag tac ctg cag ctg gat ttt acc aca aga gtg ggc atg aag Asp Glu Lys Tyr Leu Gln Leu Asp Phe Thr Thr Arg Val Gly Met Lys 545 550 555 560			1680
ctc aag gag aag aag atg gct ttt tgg atg agt ctg tac cag tct caa Leu Lys Glu Lys Lys Met Ala Phe Trp Met Ser Leu Tyr Gln Ser Gln 565 570 575			1728
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<213> Artificial Sequence			

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<223> Motif

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<223> Xaa may be Gly or Arg

<221> VARIANT

<222> 4,5,6,7,9,11,13

<223> Xaa may be any amino acid

<221> VARIANT

<222> 8

<223> Xaa may be Leu, Ile, Met or Val

<221> VARIANT

<222> 10

<223> Xaa may be Leu, Ile or Val

<221> VARIANT

<222> 15

<223> Xaa may be Ser, Thr, Ala, or Gly

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Phe Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly
1 5 10 15

<210> 5

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Motif

<221> VARIANT

<222> 1

<223> Xaa may be Glu or Asp

<221> VARIANT

<222> 5

<223> Xaa may be Tyr or Thr

<221> VARIANT

<222> 6,8

<223> Xaa may be Leu, Ile or Val

<221> VARIANT

<222> 7

<223> Asp, Asn, or Ser

<221> VARIANT

<222> 9

<223> Xaa may be Leu, Ile, Phe, Tyr, Trp or Val

<221> VARIANT

<222> (10)...(10)

<223> Xaa may be any amino acid

<221> VARIANT
<222> (11)...(11)
<223> Xaa may be Pro, Gln or Arg

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Xaa Asp Cys Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10

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<210> 6
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<212> DNA
<213> Homo sapiens
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<220>
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gtcgagccct ggccagacat gtccacaggg ttctccctcg ggtccgggac tctgggctcc 180
accaccgtgg ccggccggcgg gaccagcaca ggccggcggtt tctccctcg aacggaaacg 240
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cccccgagc cctggaaagg aatcagagat gctaccacct accccgcctgg atggagtctc 600
gctctgtcgc caggtctggag tgcagtgtca cgcattctggc tcactgtcaac ctccgcctcc 660
cggttcaag cgagtctctt gcctcagccct ctgagttgtct ggggctacag gtgcctgcag 720
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tcgtacgagg gctctgtactt ggccgcccgc gagaaaagtgg tgctgtgtt tctgcagcac 960
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gaccaggaa atgtgaccct ttccggccag tcggcggggg ccatgagcat ctcaggactg 1140
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